



1  
SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Blundell, Tom L  
Abell, Christopher  
Inoue, Tsuyoshi  
von Delft, Frank

<120> Crystal Structure

<130> 620-139

<140> US 09/820,745

<141> 2001-03-30

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 1

Leu Val Gly Asp Ser Leu Gly Met

1

5

<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 2

Val Lys Ile Glu Gly Gly

1

5

<210> 3

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

<220>  
<221> SITE  
<222> (3)  
<223> Xaa is a hydrophobic residue

<400> 3  
Gly His Xaa Gly Leu Thr Pro Gln  
1 5

<210> 4  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 4  
Gly Gly Tyr Lys Val Gln Gly  
1 5

<210> 5  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 5  
Ile Gly Ile Gly Ala Gly  
1 5

<210> 6  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 6  
Asp Gly Asn Ile Leu Val  
1 5

<400>	7															
Met	Lys	Pro	Thr	Thr	Ile	Ser	Leu	Leu	Gln	Lys	Tyr	Lys	Gln	Asp	Lys	
1				5				10			15					
Lys	Arg	Phe	Ala	Thr	Ile	Thr	Ala	Tyr	Asp	Tyr	Ser	Phe	Ala	Lys	Leu	
			20				25			30						
Phe	Ala	Asp	Glu	Gly	Leu	Asn	Val	Met	Leu	Val	Gly	Asp	Ser	Leu	Gly	
			35				40			45						
Met	Thr	Val	Gln	Gly	His	Asp	Ser	Thr	Leu	Pro	Val	Thr	Val	Ala	Asp	
			50				55			60						
Ile	Ala	Tyr	His	Thr	Ala	Ala	Val	Arg	Arg	Gly	Ala	Pro	Asn	Cys	Leu	
65					70			75					80			
Leu	Leu	Ala	Asp	Leu	Pro	Phe	Met	Ala	Tyr	Ala	Thr	Pro	Glu	Gln	Ala	
				85			90					95				
Phe	Glu	Asn	Ala	Ala	Thr	Val	Met	Arg	Ala	Gly	Ala	Asn	Met	Val	Lys	
			100			105			110							
Ile	Glu	Gly	Gly	Glu	Trp	Leu	Val	Glu	Thr	Val	Gln	Met	Leu	Thr	Glu	
		115		120			125									
Arg	Ala	Val	Pro	Val	Cys	Gly	His	Leu	Gly	Leu	Thr	Pro	Gln	Ser	Val	
130			135			140										
Asn	Ile	Phe	Gly	Gly	Tyr	Lys	Val	Gln	Gly	Arg	Gly	Asp	Glu	Ala	Gly	
145					150			155					160			
Asp	Gln	Leu	Leu	Ser	Asp	Ala	Leu	Ala	Leu	Glu	Ala	Ala	Gly	Ala	Gln	
				165			170					175				
Leu	Leu	Val	Leu	Glu	Cys	Val	Pro	Val	Glu	Leu	Ala	Lys	Arg	Ile	Thr	
			180			185			190							
Glu	Ala	Leu	Ala	Ile	Pro	Val	Ile	Gly	Ile	Gly	Ala	Gly	Asn	Val	Thr	
		195		200			205									
Asp	Gly	Gln	Ile	Leu	Val	Met	His	Asp	Ala	Phe	Gly	Ile	Thr	Gly	Gly	
210			215			220										
His	Ile	Pro	Lys	Phe	Ala	Lys	Asn	Phe	Leu	Ala	Glu	Thr	Gly	Asp	Ile	
225				230			235					240				
Arg	Ala	Ala	Val	Arg	Gln	Tyr	Met	Ala	Glu	Val	Glu	Ser	Gly	Val	Tyr	
			245			250					255					
Pro	Gly	Glu	Glu	His	Ser	Phe	His									
				260												

<210> 8  
 <211> 267  
 <212> PRT  
 <213> Schizosaccharomyces pombe

<400> 8

Met	Ser	Leu	Lys	Gln	Ile	Thr	Ile	Ser	Thr	Leu	Arg	Gln	Trp	Lys	Leu
1				5					10					15	
Ala	Asn	Lys	Lys	Phe	Ala	Cys	Ile	Thr	Ala	Tyr	Asp	Ala	Ser	Phe	Ser
			20					25					30		
Arg	Leu	Phe	Ala	Glu	Gln	Gly	Met	Pro	Val	Met	Leu	Val	Gly	Asp	Ser
		35					40					45			
Leu	Gly	Met	Thr	Ala	Gln	Gly	His	Ser	Thr	Thr	Leu	Pro	Val	Ser	Val
	50					55					60				
Glu	Asp	Ile	Ala	Tyr	His	Thr	Lys	Ser	Val	Arg	Arg	Gly	Ala	Pro	Asn
65					70					75					80
Arg	Leu	Leu	Met	Ala	Asp	Leu	Pro	Phe	Met	Ser	Tyr	Ser	Thr	Trp	Glu
				85					90					95	
Asp	Ala	Cys	Lys	Asn	Ala	Ala	Thr	Val	Met	Arg	Ala	Gly	Ala	Asn	Ile
			100					105					110		
Val	Lys	Ile	Glu	Gly	Gly	Gly	Asn	Trp	Ile	Phe	Glu	Ile	Val	Gln	Arg
	115						120					125			
Leu	Thr	Glu	Arg	Ser	Val	Pro	Val	Ala	Gly	His	Leu	Gly	Leu	Thr	Pro
	130					135					140				
Gln	Ser	Val	Asn	Ile	Phe	Gly	Gly	Tyr	Lys	Ile	Gln	Gly	Arg	Glu	Gln
145				150					155						160
Ser	Ala	Ala	Ala	Arg	Leu	Ile	Glu	Asn	Ala	Gln	Gln	Leu	Glu	Lys	Phe
				165				170						175	
Gly	Ala	Gln	Leu	Leu	Val	Leu	Glu	Cys	Ile	Pro	Glu	Ser	Leu	Ala	Glu
			180					185					190		
Gln	Ile	Thr	Lys	Thr	Ile	Ser	Ile	Pro	Thr	Ile	Gly	Ile	Gly	Ala	Gly
	195					200						205			
Lys	His	Thr	Asp	Gly	Gln	Ile	Leu	Val	Met	His	Asp	Ala	Leu	Gly	Ile
	210				215						220				
Thr	Gly	Gly	Arg	Pro	Pro	Lys	Phe	Ala	Lys	Asn	Phe	Leu	Ser	Gly	Ala
225					230					235					240
Gly	Asp	Ile	Arg	Thr	Ala	Ile	Gln	Arg	Tyr	Ile	Tyr	Glu	Val	Glu	Gln
			245					250						255	
Gly	Leu	Tyr	Pro	Ala	Glu	Glu	His	Ser	Phe	Gln					
			260					265							

<210> 9  
 <211> 349  
 <212> PRT  
 <213> *Aspergillus nidulans*

<400> 9  
 Met Thr Phe Leu Arg Ile Ala Thr Lys Arg Ala Ile Tyr Leu His Arg  
     1                    5                    10                    15  
 Pro Ala Asn Pro Ala Leu Pro Thr Ser Ser Ile Leu Pro Val Leu His  
                     20                    25                    30  
 Ser Thr Asn Val Ala Thr Arg Val Pro Ser Pro Cys Ala Ile Arg His  
             35                    40                    45  
 Ser Ser His Ser Pro Leu Gly Ala Ala Gln Ala Asn Pro Arg Lys Lys  
     50                    55                    60  
 Val Thr Met Gln Thr Leu Arg Asn Leu Tyr Lys Lys Gly Glu Pro Ile  
     65                    70                    75                    80  
 Thr Met Leu Thr Ala His Asp Phe Pro Ser Ala His Val Ala Asp Ala  
                     85                    90                    95  
 Ala Gly Met Asp Met Ile Leu Val Gly Asp Ser Leu Ala Met Val Ala  
             100                    105                    110  
 Leu Gly Met Gln Asp Thr Ser Glu Val Thr Leu Asp Asp Met Leu Val  
     115                    120                    125  
 His Cys Arg Ser Val Ala Arg Ala Ala Gln Ser Ala Phe Thr Val Ser  
     130                    135                    140  
 Asp Leu Pro Met Gly Ser Tyr Glu Val Ser Pro Glu Gln Ala Leu Gln  
     145                    150                    155                    160  
 Ser Ala Ile Arg Ile Val Lys Glu Gly Arg Val Gln Gly Val Lys Leu  
             165                    170                    175  
 Glu Gly Gly Glu Glu Met Ala Pro Ala Ile Lys Arg Ile Thr Thr Ala  
             180                    185                    190  
 Gly Ile Pro Val Val Gly His Ile Gly Leu Thr Pro Gln Arg Gln Asn  
     195                    200                    205  
 Ala Leu Gly Gly Phe Arg Val Gln Gly Lys Ser Thr Thr Asp Ala Leu  
     210                    215                    220  
 Lys Leu Leu Lys Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Met  
     225                    230                    235                    240  
 Ile Val Ile Glu Ala Val Pro Pro Glu Ile Ala Ser Ile Val Thr Gln  
             245                    250                    255  
 Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Cys Ser  
             260                    265                    270

Gly Gln Val Leu Val Gln Ile Asp Met Thr Gly Asn Phe Pro Pro Gly  
 275 280 285

Arg Phe Leu Pro Lys Phe Val Lys Gln Tyr Ala Asn Val Trp Asn Glu  
 290 295 300

Ala Leu Gln Gly Ile Gln Gln Tyr Arg Glu Glu Val Lys Ser Arg Ala  
 305 310 315 320

Tyr Pro Ala Glu Gln His Thr Tyr Pro Ile Pro Lys Glu Glu Leu Val  
 325 330 335

Glu Phe Gln Lys Ala Val Asp Glu Leu Pro Glu Glu Lys  
 340 345

<210> 10

<211> 347

<212> PRT

<213> Arabidopsis thaliana

<400> 10

Met Ala Ser Ser Leu Thr Arg Asn Cys Ser Arg Phe Ser Lys Ala Ile  
 1 5 10 15

Ser Val Arg Phe Met Ser Asn Leu Pro Glu Asn Thr Val Tyr Gly Gly  
 20 25 30

Pro Lys Pro Gln Asn Pro Asn Gln Arg Val Thr Leu Thr His Leu Arg  
 35 40 45

Gln Lys His Arg Arg Gly Glu Pro Ile Thr Val Val Thr Ala Tyr Asp  
 50 55 60

Tyr Pro Ser Ala Val His Leu Asp Thr Ala Gly Ile Asp Val Cys Leu  
 65 70 75 80

Val Gly Asp Ser Ala Ser Met Val Val His Gly His Asp Thr Thr Leu  
 85 90 95

Pro Ile Ser Leu Asp Glu Met Leu Val His Cys Arg Ala Val Ala Arg  
 100 105 110

Gly Ala Lys Arg Pro Leu Leu Val Gly Asp Leu Pro Phe Gly Thr Tyr  
 115 120 125

Glu Ser Ser Ser Ser Gln Ala Val Asp Thr Ala Val Arg Val Leu Lys  
 130 135 140

Glu Gly Gly Met Asp Ala Ile Lys Leu Glu Gly Gly Ser Ala Ser Arg  
 145 150 155 160

Ile Thr Ala Ala Lys Ala Ile Val Glu Ala Gly Ile Ala Val Ile Gly  
 165 170 175

His Val Gly Leu Thr Pro Gln Ala Ile Ser Val Leu Gly Gly Phe Arg  
 180 185 190

Pro Gln Gly Arg Asn Ile Ala Ser Ala Val Lys Val Val Glu Thr Ala  
 195 200 205

Met Ala Leu Gln Glu Ala Gly Cys Phe Ser Val Val Leu Glu Cys Val  
 210 215 220

Pro Pro Pro Val Ala Ala Ala Ala Thr Ser Ala Leu Lys Ile Pro Thr  
 225 230 235 240

Ile Gly Ile Gly Ala Gly Pro Phe Cys Ser Gly Gln Val Leu Val Tyr  
 245 250 255

His Asp Leu Leu Gly Met Met Gln His Pro His His Ala Lys Val Thr  
 260 265 270

Pro Lys Phe Cys Lys Gln Tyr Ala Asn Val Gly Glu Val Ile Asn Lys  
 275 280 285

Ala Leu Met Glu Tyr Lys Glu Glu Val Ser Lys Lys Val Phe Pro Gly  
 290 295 300

Pro Ser His Ser Pro Tyr Lys Ile Thr Ala Ser Glu Leu Asp Gly Phe  
 305 310 315 320

Leu Thr Glu Leu Gln Lys Leu Gly Phe Asp Lys Ala Ala Ser Ala Ala  
 325 330 335

Ala Leu Ala Ala Glu Asn Met Glu Pro Ser Lys  
 340 345

<210> 11  
 <211> 312  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 11  
 Met Asn Ile Met Lys Arg Gln Leu Cys Thr Ser Ser Lys Arg Phe Phe  
 1 5 10 15

Ser Thr Ala Lys Asn Val Val Lys Tyr Asn Thr Ile Gln Asp Ile Arg  
 20 25 30

Asn Lys Tyr Phe Thr Gly Thr Pro Leu Ser Met Cys Thr Ala Tyr Asp  
 35 40 45

Phe Ile Thr Ala Thr Trp Val Asn Lys Ala Asn Cys Asp Leu Leu Leu  
 50 55 60

Val Gly Asp Ser Leu Ala Met Thr Ser Leu Gly Tyr Asp Ser Thr Ile  
 65 70 75 80

Thr Leu Ser Leu Asn Glu Phe Lys Tyr His Val Ala Ser Val Cys Arg  
 85 90 95

Ala Glu Gly Ser Ser Met Val Val Val Asp Met Pro Phe Gly Thr Phe  
 100 105 110

Glu Ser Gly Ile Ser Asp Gly Leu Lys Asn Ala Ile Asp Ile Met Lys  
 115 120 125  
 Leu Asp Ser Lys Val Thr Ser Val Lys Val Glu Val Gly Ser Tyr Thr  
 130 135 140  
 Lys Asp Lys Tyr Ala Met Lys Phe Ile Glu Glu Leu Cys Ser Arg Gly  
 145 150 155 160  
 Ile Pro Val Met Ala His Ile Gly Leu Thr Pro Gln Lys Val His Ser  
 165 170 175  
 Leu Gly Gly Tyr Lys Val Gln Gly Ser Lys Ser Leu Leu Gln Met Gln  
 180 185 190  
 Glu Leu Tyr Glu Thr Ala Met Gln Leu Gln Lys Ile Gly Cys Trp Ser  
 195 200 205  
 Ile Leu Ile Glu Cys Val Pro His Lys Met Ala Gln Phe Ile Thr Ser  
 210 215 220  
 Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Thr Ser  
 225 230 235 240  
 Gly Gln Val Leu Val Ile Ser Asp Leu Leu Gly Met Gln Gly Asp Ser  
 245 250 255  
 Val Pro Lys Phe Val Lys Gln Ala Val Asn Met Thr Asp Ile Ala Thr  
 260 265 270  
 Gln Gly Leu Lys Glu Tyr Ile Ala Ser Val Glu Asp Arg Thr Phe Pro  
 275 280 285  
 Glu Arg Gly Thr His Thr Phe Lys Val Lys Glu Asp Leu Trp Asn Glu  
 290 295 300  
 Phe Leu Ser Ser Ile Asn Glu Lys  
 305 310

<210> 12

<211> 281

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus

<220>

<221> SITE

<222> 1..4, 6..8, 10..22, 27..29, 31..39, 41, 50..52, 54..56

<223> Xaa is uncertain

<220>

<221> SITE

<222> 59, 62..64, 66, 67, 69..71, 73, 76..81, 83, 88, 89

<223> Xaa is uncertain



<220>  
 <221> SITE  
 <222> 91..96, 97..100, 102, 103, 105..108, 110..113, 120..133  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 135..138, 140, 142, 145, 151..155, 163, 165..171  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 173..175, 177, 179..181, 185, 186, 191, 194, 195  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 198..200, 202..205, 208, 215..217, 224, 225, 227, 228  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 230..242, 246, 248..258, 260..262, 264..266, 268..271  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 274..277, 279..281  
 <223> Xaa is uncertain

<400> 12  
 Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
   1                  5                  10                  15  
 Xaa Xaa Xaa Xaa Xaa Xaa Thr Ala Tyr Asp Xaa Xaa Xaa Ala Xaa Xaa  
                   20                  25                  30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Val Gly Asp Ser Leu Gly  
                   35                  40                  45  
 Met Xaa Xaa Xaa Gly Xaa Xaa Xaa Thr Leu Xaa Val Thr Xaa Xaa Xaa  
      50                  55                  60  
 Ile Xaa Xaa His Xaa Xaa Xaa Val Xaa Arg Gly Xaa Xaa Xaa Xaa Xaa  
   65                  70                  75                  80  
 Xaa Leu Xaa Asp Leu Pro Phe Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa  
                   85                  90                  95  
 Ala Xaa Xaa Xaa Ala Xaa Xaa Val Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa  
                   100                  105                  110  
 Xaa Val Lys Ile Glu Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
   115                  120                  125  
 Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Val Xaa Val Xaa Gly His  
   130                  135                  140

Xaa Gly Leu Thr Pro Gln Xaa Xaa Xaa Xaa Xaa Gly Gly Tyr Lys Val	
145	150 155 160
Gln Gly Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Ala	
	165 170 175
Xaa Ala Xaa Xaa Xaa Ala Gly Ala Xaa Xaa Leu Val Leu Glu Xaa Val	
	180 185 190
Pro Xaa Xaa Leu Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Ile Pro Xaa	
	195 200 205
Ile Gly Ile Gly Ala Gly Xaa Xaa Xaa Asp Gly Gln Ile Leu Val Xaa	
	210 215 220
Xaa Asp Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
225	230 235 240
Xaa Xaa Pro Lys Phe Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
	245 250 255
Xaa Xaa Ala Xaa Xaa Xaa Tyr Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Tyr	
	260 265 270
Pro Xaa Xaa Xaa Xaa His Xaa Xaa Xaa	
	275 280